

Length=1255

Score = 2602 bits (6744), Expect = 0.0, Method: Compositional matrix adjust.  
 Identities = 1255/1255 (100%), Positives = 1255/1255 (100%), Gaps = 0/1255 (0%)

Query	1	MFIFLLFLTLTSGSDLRCTTFDDVQAPNYTQHTSSMRGVVYPDEIFRSDTLYLTQDLFL	60
Sbjct	1	MFIFLLFLTLTSGSDLRCTTFDDVQAPNYTQHTSSMRGVVYPDEIFRSDTLYLTQDLFL	60
Query	61	PFFYSNVITGFGHTINHITFGNPVIFPKDGIYFAATEKSNVVRGWVFGSTMMNKSQSVIIINNS	120
Sbjct	61	PFFYSNVITGFGHTINHITFGNPVIFPKDGIYFAATEKSNVVRGWVFGSTMMNKSQSVIIINNS	120
Query	121	TNVVIRACNELCNDPPFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK	180
Sbjct	121	TNVVIRACNELCNDPPFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK	180
Query	181	HLREFVFKNKDGLFVYKGYQPIDVVRDLPSGFGNTLKPFIKPLPLGINITNFRAILTAFSP	240
Sbjct	181	HLREFVFKNKDGLFVYKGYQPIDVVRDLPSGFGNTLKPFIKPLPLGINITNFRAILTAFSP	240
Query	241	AQDIWGTSAAYFVGYLKPTTFMLKYDENGITIDAVDCSQNPLAELKCSVKSEFIDKGIY	300
Sbjct	241	AQDIWGTSAAYFVGYLKPTTFMLKYDENGITIDAVDCSQNPLAELKCSVKSEFIDKGIY	300
Query	301	QTSNFRVPSGDDVRFENITNLCPFGEVFNATKFPSSVYAWERKKISNCVADYSVLYNSTF	360
Sbjct	301	QTSNFRVPSGDDVRFENITNLCPFGEVFNATKFPSSVYAWERKKISNCVADYSVLYNSTF	360
Query	361	FSTFKCYGVSAATKLNLDLCSNVYADSFVVGKDDVRQIAPGQTGVIADYNYKLPDDFMGCV	420
Sbjct	361	FSTFKCYGVSAATKLNLDLCSNVYADSFVVGKDDVRQIAPGQTGVIADYNYKLPDDFMGCV	420
Query	421	LAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVFSPDGKPCPTPALNCYWFPLND	480
Sbjct	421	LAWNTRNIDATSTGNYNYKYRYLRHGKLRPFERDISNVFSPDGKPCPTPALNCYWFPLND	480
Query	481	YGFYTTTIGIGYQPIRVVVLSELLNAPATVCGPKLSTDLIKNQCVNFNGLTGTGVLTP	540
Sbjct	481	YGFYTTTIGIGYQPIRVVVLSELLNAPATVCGPKLSTDLIKNQCVNFNGLTGTGVLTP	540
Query	541	SSKRFQFPQQGRDVSDFTSVDRPKTSEILDSPCSFGGVSVITPGTNASSEVAVLYQD	600
Sbjct	541	SSKRFQFPQQGRDVSDFTSVDRPKTSEILDSPCSFGGVSVITPGTNASSEVAVLYQD	600
Query	601	VNCTDVSTAIAHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSEYCDIPIGAGICASY	660
Sbjct	601	VNCTDVSTAIAHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSEYCDIPIGAGICASY	660
Query	661	HTVSLRLSTSQKSIYAYTMSLGADSSIAYSNNITAIPTNFSISITTEVMEVMSAKTSVDC	720
Sbjct	661	HTVSLRLSTSQKSIYAYTMSLGADSSIAYSNNITAIPTNFSISITTEVMEVMSAKTSVDC	720
Query	721	NMYICGDSSTECANLLQYGSFCTQLNRALSGIAAEQDRNTREVAQVKQMYKPTLKYFG	780
Sbjct	721	NMYICGDSSTECANLLQYGSFCTQLNRALSGIAAEQDRNTREVAQVKQMYKPTLKYFG	780
Query	781	GFNFSQILDPDLKPKTRSFIEDLLFNKVTLDADAGFMKYQGECLGDINARDLICAQKFNGL	840
Sbjct	781	GFNFSQILDPDLKPKTRSFIEDLLFNKVTLDADAGFMKYQGECLGDINARDLICAQKFNGL	840
Query	841	TVLPPELLTDDMIAAYTAALVSGTATAGWTFGAGAAQIPFAMQAYRFGNIGVTONVLYE	900
Sbjct	841	TVLPPELLTDDMIAAYTAALVSGTATAGWTFGAGAAQIPFAMQAYRFGNIGVTONVLYE	900
Query	901	NQKQIANQNFKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN	960
Sbjct	901	NQKQIANQNFKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN	960
Query	961	DILSRLDKVEAEVQIDRLITGRQLSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK	1020
Sbjct	961	DILSRLDKVEAEVQIDRLITGRQLSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK	1020
Query	1021	RVDFCGKGYHLMSFPQAPAHGVVFLHVTVYVPSQRRNFTTAPAIHEGKAYFPREGVVFVN	1080
Sbjct	1021	RVDFCGKGYHLMSFPQAPAHGVVFLHVTVYVPSQRRNFTTAPAIHEGKAYFPREGVVFVN	1080
Query	1081	GTSWFITQRNFFSPQIITDNTFVSGNCDVIGIINNTYDPLQPELDSFKKEELDKYFKN	1140
Sbjct	1081	GTSWFITQRNFFSPQIITDNTFVSGNCDVIGIINNTYDPLQPELDSFKKEELDKYFKN	1140
Query	1141	HTSPDVLGDLSIGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL	1200
Sbjct	1141	HTSPDVLGDLSIGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL	1200

Sbjct	1141	HTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL	1200
Query	1201	GFIAGLIAIVMVTILLCCMTSCCSCCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT	1255
		GFIAGLIAIVMVTILLCCMTSCCSCCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT	
Sbjct	1201	GFIAGLIAIVMVTILLCCMTSCCSCCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT	1255